

AMENDMENT TO THE SPECIFICATION

At page 19, lines 11-14, please amend the paragraph as follows.

Fig. 6A is a schematic illustration showing the alignment of the NPR1 amino acid sequence polypeptide (amino acids 323-371 (SEQ ID NO: 4) and amino acids 262-289 (SEQ ID NO: 6)) with the mouse ankyrin 3 (ANKB) polypeptide (amino acids 740-788 (SEQ ID NO: 5) and amino acids 313-340 (SEQ ID NO: 7)). Two regions producing the highest scoring pairs (smallest sum probability = 0.0004) generated using a BLAST search are shown. The identical and similar amino acids (+) are highlighted in bold, circled letters

At page 19, lines 15-22, please amend the paragraph as follows.

Fig. 6B is a schematic illustration showing the alignment of the ankyrin repeats in NPR1 (amino acids 265-297 (SEQ ID NO: 8), 294-326 (SEQ ID NO: 9), 328-360 (SEQ ID NO: 10), and 361-393 (SEQ ID NO: 11)) with the ankyrin repeat consensus (SEQ ID NO: 12) derived from Michael and Bennett (Trends in Cell Biology 2:127-129, 1992) and Bork (Proteins: Structure, Function, and Genetics 17:363-374, 1993). Since there are a few non-overlapping amino acids between the two derived consensus sequences, both are presented. In the consensus derived from Bork, the conserved features are indicated: t, turn-like or polar; o, S/T; h, hydrophobic; capitals, conserved amino acids. Those amino acids identical to the consensus are highlighted in bold, circled letters.